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SEQUENCE LISTING

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Deak, Maria

<120> Methods

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<140> US 09/868,131
<141> 2001-06-14

<150> PCT/GB99/04232
<151> 1999-12-14

<150> GB 9919676.8
<151> 1999-08-19

<150> US 60/112,217
<151> 1998-12-14

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<170> PatentIn Ver. 2.0

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Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
35 40 45

Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
50 55 60

Val Leu Gln Lys Lys Ser Ile Leu Lys Lys Lys Glu Gln Ser His Ile
65 70 75 80

Met Ala Glu Arg Ser Val Leu Leu Lys Asn Val Arg His Pro Phe Leu
85 90 95

Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val
100 105 110

Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu
115 120 125

Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Val Ala
130 135 140

Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu
145 150 155 160

Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr
165 170 175

Asp Phe Gly Leu Cys Lys Glu Gly Val Glu Pro Glu Asp Thr Thr Ser
180 185 190

Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
195 200 205

Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
210 215 220

Tyr Glu Met Leu His Gly Leu Pro Pro Phe Tyr Ser Gln Asp Val Ser
225 230 235 240

Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
245 250 255

Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Ser Leu Leu His Lys Asp
260 265 270

Gln Arg Gln Arg Leu Gly Ser Lys Ala Asp Phe Leu Glu Ile Lys Asn
275 280 285

His Val Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
290 295 300

Leu Thr Pro Pro Phe Asn Pro Asn Val Thr Gly Pro Ala Asp Leu Lys
305 310 315 320

His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
325 330 335

Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
340 345 350

Leu Gly Phe Ser Tyr Ala Pro Glu Asp Asp Asp Ile Leu Asp Cys
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<213> Mus musculus

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             20                  25                  30

Thr Asp Phe Asp Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys
         35                  40                  45

Val Leu Leu Ala Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys
     50                  55                  60

Val Leu Gln Lys Lys Ser Ile Leu Lys Asn Lys Glu Gln Asn His Ile
 65                  70                  75                  80

Met Ala Glu Arg Asn Val Leu Leu Lys Asn Val Arg His Pro Phe Leu
                85                  90                  95

Val Gly Leu Arg Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val
            100                 105                 110
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Leu Asp Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu
115 120 125

Arg Arg Phe Leu Glu Pro Arg Ala Arg Phe Tyr Thr Ala Glu Val Ala
130 135 140

Ser Ala Ile Gly Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu
145 150 155 160

Lys Pro Glu Asn Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr
165 170 175

Asp Phe Gly Leu Cys Lys Glu Cys Val Glu Pro Glu Glu Thr Thr Ser
180 185 190

Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys
195 200 205

Glu Pro Tyr Asp Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu
210 215 220

Tyr Glu Met Leu His Gly Leu Pro Pro Phe Phe Asn Thr Asp Val Ala
225 230 235 240

Gln Met Tyr Glu Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly
245 250 255

Arg Thr Val Ala Ala Cys Asp Leu Leu Gln Gly Leu Leu His Lys Asp
260 265 270

Gln Arg Gln Arg Leu Gly Ser Lys Glu Asp Phe Leu Asp Ile Lys Asn
275 280 285

His Met Phe Phe Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg
290 295 300

Leu Thr Pro Pro Phe Asn Pro Asn Val Glu Gly Pro Ala Asp Leu Lys
305 310 315 320

His Phe Asp Pro Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly
325 330 335

Cys Thr Pro Asp Thr Val Ala Ser Ser Ser Gly Ala Ser Ser Ala Phe
340 345 350

Leu Gly Phe Ser Tyr Ala Gln Asp Asp Asp Asp Ile Leu Asp Ser
355 360 365

<210> 4

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<213> h. sapiens

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             20                  25                  30

Asn Leu Val Arg Tyr Pro Glu Leu Tyr Asn His Pro Asp Val Arg Ala
         35                  40                  45

Phe Leu Gln Met Asp Ser Pro Lys His Gln Ser Asp Pro Ser Glu Asp
     50                  55                  60

Glu Asp Glu Arg Ser Ser Gln Lys Leu His Ser Thr Ser Gln Asn Ile
 65                  70                  75                  80

Asn Leu Gly Pro Ser Gly Asn Pro His Ala Lys Pro Thr Asp Phe Asp
                 85                  90                  95

Phe Leu Lys Val Ile Gly Lys Gly Ser Phe Gly Lys Val Leu Leu Ala
            100                 105                 110

Lys Arg Lys Leu Asp Gly Lys Phe Tyr Ala Val Lys Val Leu Gln Lys
        115                 120                 125

Lys Ile Val Leu Asn Arg Lys Glu Gln Lys His Ile Met Ala Glu Arg
    130                 135                 140

Asn Val Leu Leu Lys Asn Val Lys His Pro Phe Leu Val Gly Leu His
145                 150                 155                 160

Tyr Ser Phe Gln Thr Thr Glu Lys Leu Tyr Phe Val Leu Asp Phe Val
                165                 170                 175

Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu Arg Ser Phe Pro
            180                 185                 190

Glu His Arg Ala Arg Phe Tyr Ala Ala Glu Ile Ala Ser Ala Leu Gly
        195                 200                 205

Tyr Leu His Ser Ile Lys Ile Val Tyr Arg Asp Leu Lys Pro Glu Asn
    210                 215                 220

Ile Leu Leu Asp Ser Val Gly His Val Val Leu Thr Asp Phe Gly Leu
225                 230                 235                 240

Cys Lys Glu Gly Ile Ala Ile Ser Asp Thr Thr Thr Thr Phe Cys Gly
                245                 250                 255
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Thr Pro Glu Tyr Leu Ala Pro Glu Val Ile Arg Lys Gln Pro Tyr Asp
260 265 270

Asn Thr Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu
275 280 285

Tyr Gly Leu Pro Pro Phe Tyr Cys Arg Asp Val Ala Glu Met Tyr Asp
290 295 300

Asn Ile Leu His Lys Pro Leu Ser Leu Arg Pro Gly Val Ser Leu Thr
305 310 315 320

Ala Trp Ser Ile Leu Glu Glu Leu Leu Glu Lys Asp Arg Gln Asn Arg
325 330 335

Leu Gly Ala Lys Glu Asp Phe Leu Glu Ile Gln Asn His Pro Phe Phe
340 345 350

Glu Ser Leu Ser Trp Ala Asp Leu Val Gln Lys Lys Ile Pro Pro Pro
355 360 365

Phe Asn Pro Asn Val Ala Gly Pro Asp Asp Ile Arg Asn Phe Asp Thr
370 375 380

Ala Phe Thr Glu Glu Thr Val Pro Tyr Ser Val Cys Val Ser Ser Asp
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<212> DNA

<213> h. sapiens

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tgcctgaagc cctggatggg cggagctgac cccccaacac caactctatc atgcctgctc 360

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<213> h. sapiens

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tataaagttc tggtttcagt gggaagaagt gaatggtttg tcttcaggag atatgcagag 180

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gataaatcac tgtttgaaat atttggttca tggtatgatc gaaatgtaaa agcataatta 2040

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aggctaaggc aggagaatcg cttgaacccg ggaggcggag gttgcagtga gccgagatcg 2340

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<213> h. sapiens

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cagccctcca gggccaatgg gaacatcaac ctggggcctt cagccaaccc aaatgcccag 180

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<212> PRT

<213> h. sapiens

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Cys Thr Gly Arg Gly Gly Trp Arg Gly Gln Trp Cys Leu Lys Pro Trp
20 25 30

Met Gly Gly Ala Asp Pro Pro Thr Pro Thr Leu Ser Cys Leu Leu Leu
35 40 45

Pro Val Pro Pro Glu Leu Pro Asp His Cys Tyr Arg Met Asn Ser Ser
50 55 60

Pro Ala Gly Thr Pro Ser Pro Gln Pro Ser Arg Ala Asn Gly Asn Ile
65 70 75 80

Asn Leu Gly Pro Ser Ala Asn Pro Asn Ala Gln Pro Thr Asp Phe Asp
85 90 95

Phe Leu Lys Val Ile Gly Lys Gly Asn Tyr Gly Lys Val Leu Leu Ala
100 105 110

Lys Arg Lys Ser Asp Gly Ala Phe Tyr Ala Val Lys Val Leu Gln Lys
115 120 125

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Lys Ser Ile Leu Lys Lys Lys Glu Gln Ser His Ile Met Ala Glu Arg
    130                 135                 140

Ser Val Leu Leu Lys Asn Val Arg His Pro Phe Leu Val Gly Leu Arg
145                 150                 155                 160

Tyr Ser Phe Gln Thr Pro Glu Lys Leu Tyr Phe Val Leu Asp Tyr Val
                165                 170                 175

Asn Gly Gly Glu Leu Phe Phe His Leu Gln Arg Glu Arg Arg Phe Leu
            180                 185                 190

Glu Pro Arg Ala Arg Phe Tyr Ala Ala Glu Val Ala Ser Ala Ile Gly
        195                 200                 205

Tyr Leu His Ser Leu Asn Ile Ile Tyr Arg Asp Leu Lys Pro Glu Asn
    210                 215                 220

Ile Leu Leu Asp Cys Gln Gly His Val Val Leu Thr Asp Phe Gly Leu
225                 230                 235                 240

Cys Lys Glu Gly Val Glu Pro Glu Asp Thr Thr Ser Thr Phe Cys Gly
                245                 250                 255

Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Arg Lys Glu Pro Tyr Asp
            260                 265                 270

Arg Ala Val Asp Trp Trp Cys Leu Gly Ala Val Leu Tyr Glu Met Leu
        275                 280                 285

His Gly Leu Pro Pro Phe Tyr Ser Gln Asp Val Ser Gln Met Tyr Glu
    290                 295                 300

Asn Ile Leu His Gln Pro Leu Gln Ile Pro Gly Gly Arg Thr Val Ala
305                 310                 315                 320

Ala Cys Asp Leu Leu Gln Ser Leu Leu His Lys Asp Gln Arg Gln Arg
                325                 330                 335

Leu Gly Ser Lys Ala Asp Phe Leu Glu Ile Lys Asn His Val Phe Phe
            340                 345                 350

Ser Pro Ile Asn Trp Asp Asp Leu Tyr His Lys Arg Leu Thr Pro Pro
        355                 360                 365

Phe Asn Pro Asn Val Thr Gly Pro Ala Asp Leu Lys His Phe Asp Pro
    370                 375                 380

Glu Phe Thr Gln Glu Ala Val Ser Lys Ser Ile Gly Cys Thr Pro Asp
385                 390                 395                 400

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<211> 72

<212> DNA

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ggctgctaag ggc 73

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<212> DNA

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<210> 11

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PCR PRIMER

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<210> 12

<211> 15

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:PCR PRIMER

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cgttagtgga tccga 15

<210> 13

<211> 27

<212> DNA

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<210> 14

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<223> Description of Artificial Sequence:PCR PRIMER

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gctgggcatt tgggttggct gaaggcc 27

<210> 16

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:PCR PRIMER

<400> 16

aacatccgtt tttggttgga ttgc 24

<210> 17

<211> 20

<212> DNA

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<223> Description of Artificial Sequence:PCR PRIMER

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<210> 18

<211> 25

<212> DNA

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<210> 19

<211> 26

<212> DNA

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<223> Description of Artificial Sequence:PCR PRIMER

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<210> 20

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Arg Pro Lys Thr Ser Ser Phe
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Arg Pro Arg Thr Ser Ser Val
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Arg Pro Arg Thr Ser Ser Lys
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